

SEQUENCE LISTING

<110> CHUGAI SEIYAKU KABUSHIKI KAISHA

<120> Agonist antibody

<130> FP1009

<141> 2001-04-17

<150> JP2000-115246

<151> 2000-04-17

<150> JP2000-321821

<151> 2000-10-20

<150> JP2000-321822

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<151> 2001-03-12

<160> 109

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<211> 27

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<400> 1

ccatcctaat acgactcact atagggc 27

<210> 2

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 2

ggatcccggg tggatggtgg gaagatg 27

<210> 3

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 3

ggatcccggg ccagtggata gacagatg 28

<210> 4

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 4

ggatcccggg agtggataga ccgatg 26

<210> 5

<211> 394

<212> DNA

<213> Mus

<220>

<221> CDS

<222> (1)...(393)

<223> pGEM-MIL. 1-57;signal peptide, 58-394;mature peptide

<400> 5

atg aag ttg cct gtt agg ctg ttg gtg ctg atg ttc tgg att cct 45

Met Lys Leu Pro Val Arg Leu Leu Val Leu Met Phe Trp Ile Pro

5

10

15

gcg tcc agc agt gat gtt gtg atg acc caa act cca ctc tcc ctg 90

Ala Ser Ser Ser Asp Val Val Met Thr Gln Thr Pro Leu Ser Leu

20

25

30

cct gtc agt ctt gga gat caa gcc tcc atc tct tgc aga tct agt 135

Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser

35

40

45

cag agc ctt cta cac agt aaa gga aac acc tat tta caa tgg tac 180

Gln Ser Leu Leu His Ser Lys Gly Asn Thr Tyr Leu Gln Trp Tyr

50

55

60

cta cag aag cca ggc cag tct cca aag ctc ctg atc tac aaa gtt 225

Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val

65

70

75

tcc aac cga ttt tct ggg gtc cca gac agg ttc agt ggc agt gga 270

Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly

80

85

90

tca ggg aca gat ttc aca ctc aag atc agc aga gtg gag gct gag 315

Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu

95

100

105

gat ctg gga gtt tat ttc tgc tct caa agt aca cat gtt ccg tac 360

Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser Thr His Val Pro Tyr

110

115

120

acg tcc gga ggg ggg acc aag ctg gaa ata aaa c 394

Thr Ser Gly Gly Gly Thr Lys Leu Glu Ile Lys

125

130

<210> 6

<211> 409

<212> DNA

<213> Mus

<220>

<221> CDS

<222> (1)...(408)

<223> pGEM-M1H. 1-57;signal peptide, 58-409;mature peptide

<400> 6

atg gaa tgg agc tgg ata ttt ctc ttc ctc ctg tca gga act gca 45

Met Glu Trp Ser Trp Ile Phe Leu Phe Leu Leu Ser Gly Thr Ala

5

10

15

ggt gtc cac tcc cag gtc cag ctg cag cag tct gga cct gac ctg 90

Gly Val His Ser Gln Val Gln Leu Gln Gln Ser Gly Pro Asp Leu

10

25

30

gta aag cct ggg gct tca gtg aag atg tcc tgc aag gct tct gga 135

Val Lys Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly

35

40

45

tac acc ttc gtt aac cat gtt atg cac tgg gtg aag cag aag cca 180

Tyr Thr Phe Val Asn His Val Met His Trp Val Lys Gln Lys Pro

50

55

60

ggg cag ggc ctt gag tgg att gga tat att tat cct tac aat gat 225

Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Tyr Pro Tyr Asn Asp

65

70

75

ggt act aag tac aat gag aag ttc aag ggc aag gcc aca ctg act 270

Gly Thr Lys Tyr Asn Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr

80

85

90

tca gag aaa tcc tcc agc gca gcc tac atg gag ctc agc agc ctg 315

Ser Glu Lys Ser Ser Ser Ala Ala Tyr Met Glu Leu Ser Ser Leu

95

100

105

gcc tct gag gac tct gcg gtc tac tac tgt gca aga ggg ggt tac 360

Ala Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala Arg Gly Gly Tyr

110

115

120

tat agt tac gac gac tgg ggc caa ggc acc act ctc aca gtc tcc 405

Tyr Ser Tyr Asp Asp Trp Gly Gln Gly Thr Thr Leu Thr Val Ser

125

130

135

tca g 409

Ser

<210> 7

<211> 394

<212> DNA

<213> Mus

<220>

<221> CDS

<222> (1)...(393)

<223> pGEM-M2L. 1-57;signal peptide, 58-394;mature peptide

<400> 7

atg aag ttg cct gtt agg ctg ttg gtg ctg atg ttc tgg att cct 45

Met Lys Leu Pro Val Arg Leu Leu Val Leu Met Phe Trp Ile Pro

5	10	15	
ggt tcc agc agt gat gtt gtg atg acc caa agt cca ctc tcc ctg 90			
Gly Ser Ser Ser Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu			
20	25	30	
cct gtc agt ctt gga gat caa gcc tcc atc tct tgc aga tca agt 135			
Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser			
35	40	45	
cag agc ctt gtg cac agt aat gga aag acc tat tta cat tgg tac 180			
Gln Ser Leu Val His Ser Asn Gly Lys Thr Tyr Leu His Trp Tyr			
50	55	60	
ctg cag aag cca ggc cag tct cca aaa ctc ctg atc tac aaa gtt 225			
Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val			
65	70	75	
tcc aac cga ttt tct ggg gtc cca gac agg ttc agt ggc agt gga 270			
Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly			
80	85	90	
tca gtg aca gat ttc aca ctc atg atc agc aga gtg gag gct gag 315			
Ser Val Thr Asp Phe Thr Leu Met Ile Ser Arg Val Glu Ala Glu			
95	100	105	
gat ctg gga gtt tat ttc tgc tct caa agt aca cat gtt ccg tac 360			
Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser Thr His Val Pro Tyr			
110	115	120	
acg ttc gga ggg ggg acc aag ctg gaa ata aaa c 394			
Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys			
125	130		

<210> 8

<211> 409

<212> DNA

<213> Mus

<220>

<221> CDS

<222> (1)...(408)

<223> pGEM-M2H. 1-57;signal peptide, 58-409;mature peptide

<400> 8

atg gaa tgg agc tgg ata ttt ctc ttc ctc ctg tca gga act gca 45

Met Glu Trp Ser Trp Ile Phe Leu Phe Leu Leu Ser Gly Thr Ala

5

10

15

ggt gtc cac tcc cag gtc cag ctg cag cag tct gga cct gaa ctg 90

Gly Val His Ser Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu

20

25

30

gta aag cct ggg gct tca gtg aag atg tcc tgc aag gct tct gga 135

Val Lys Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly

35

40

45

tac acc ttc gct aac cat gtt att cac tgg gtg aag cag aag cca 180

Tyr Thr Phe Ala Asn His Val Ile His Trp Val Lys Gln Lys Pro

50

55

60

ggg cag ggc ctt gag tgg att gga tat att tat cct tac aat gat 225

Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Tyr Pro Tyr Asn Asp

65

70

75

ggt act aag tat aat gag aag ttc aag gac aag gcc act ctg act 270

Gly Thr Lys Tyr Asn Glu Lys Phe Lys Asp Lys Ala Thr Leu Thr

80

85

90

tca gac aaa tcc tcc acc aca gcc tac atg gac ctc agc agc ctg 315

Ser Asp Lys Ser Ser Thr Thr Ala Tyr Met Asp Leu Ser Ser Leu

95

100

105

gcc tct gag gac tct gcg gtc tat tac tgt gca aga ggg ggt tac 360

Ala Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala Arg Gly Gly Tyr

110

115

120

tat act tac gac gac tgg ggc caa ggc acc act ctc aca gtc tcc 405

Tyr Thr Tyr Asp Asp Trp Gly Gln Gly Thr Thr Leu Thr Val Ser

125

130

135

tca g 409

Ser

<210> 9

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 9

cccaagcttc caccatgaag ttgcctgtta gg 32

<210> 10

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 10

cccaagcttc caccatggaa tggagctgga ta 32

<210> 11

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 11

cgcggatcca ctcacgtttt atttccagct tggc 34

<210> 12

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 12

cgcggatcca ctcacctgag gagactgtga gagg 34

<210> 13

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 13

catgccatgg cgcaggtcca gctgcagcag 30

<210> 14

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 14

accaccacct gaggagactg tgagagt 27

<210> 15

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 15

gtctcctcag gtggtggtgg ttcgggt 27

<210> 16

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 16

cacaacatcc gatccgccac caccga 27

<210> 17

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 17

ggcggatcgg atgttgtgat gacccaa 27

<210> 18

<211> 57

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 18

cgggaattct cattatttat cgtcatcgtc ttgtagtct tttatttcca gcttggt 57

<210> 19

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Linker amino acid sequence and nucleotide sequence

<400> 19

ggt ggt ggt ggt tcg ggt ggt ggt ggt tcg ggt ggt ggc gga tcg 45

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

5

10

15

<210> 20

<211> 828

<212> DNA

<213> Mus

<220>

<221> CDS

<222> (1)...(826)

<223> pscM1. MABL1-scFv

<400> 20

atg aaa tac cta ttg cct acg gca gcc gct gga ttg tta tta ctc 45

Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu

5 10 15

gct gcc caa cca gcc atg gcg cag gtc cag ctg cag cag tct gga 90

Ala Ala Gln Pro Ala Met Ala Gln Val Gln Leu Gln Gln Ser Gly

20 25 30

cct gac ctg gta aag cct ggg gct tca gtg aag atg tcc tgc aag 135

Pro Asp Leu Val Lys Pro Gly Ala Ser Val Lys Met Ser Cys Lys

35 40 45

gct tct gga tac acc ttc gtt aac cat gtt atg cac tgg gtg aag 180

Ala Ser Gly Tyr Thr Phe Val Asn His Val Met His Trp Val Lys

50 55 60

cag aag cca ggg cag ggc ctt gag tgg att gga tat att tat cct 225

Gln Lys Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Tyr Pro

65 70 75

tac aat gat ggt act aag tac aat gag aag ttc aag ggc aag gcc 270

Tyr Asn Asp Gly Thr Lys Tyr Asn Glu Lys Phe Lys Gly Lys Ala

80 85 90

aca ctg act tca gag aaa tcc tcc agc gca gcc tac atg gag ctc 315

Thr Leu Thr Ser Glu Lys Ser Ser Ser Ala Ala Tyr Met Glu Leu

95 100 105

agc agc ctg gcc tct gag gac tct gcg gtc tac tac tgt gca aga 360

Ser Ser Leu Ala Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala Arg

110

115

120

ggg ggt tac tat agt tac gac gac tgg ggc caa ggc acc act ctc 405

Gly Gly Tyr Tyr Ser Tyr Asp Asp Trp Gly Gln Gly Thr Thr Leu

125

130

135

aca gtc tcc tca ggt ggt ggt ggt tcg ggt ggt ggt ggt tcg ggt 450

Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly

140

145

150

ggt ggc gga tcg gat gtt gtg atg acc caa act cca ctc tcc ctg 495

Gly Gly Gly Ser Asp Val Val Met Thr Gln Thr Pro Leu Ser Leu

155

160

165

cct gtc agt ctt gga gat caa gcc tcc atc tct tgc aga tct agt 540

Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser

170

175

180

cag agc ctt cta cac agt aaa gga aac acc tat tta caa tgg tac 585

Gln Ser Leu Leu His Ser Lys Gly Asn Thr Tyr Leu Gln Trp Tyr

185

190

195

cta cag aag cca ggc cag tct cca aag ctc ctg atc tac aaa gtt 630

Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val

200

205

210

tcc aac cga ttt tct ggg gtc cca gac agg ttc agt ggc agt gga 675

Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly

215

220

225

tca ggg aca gat ttc aca ctc aag atc agc aga gtg gag gct gag 720

Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu

230

235

240

gat ctg gga gtt tat ttc tgc tct caa agt aca cat gtt ccg tac 765

Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser Thr His Val Pro Tyr

245

250

255

acg tcc gga ggg ggg acc aag ctg gaa ata aaa gac tac aaa gac 810

Thr Ser Gly Gly Gly Thr Lys Leu Glu Ile Lys Asp Tyr Lys Asp

260

265

270

gat gac gat aaa taa tga 828

Asp Asp Asp Lys

<210> 21

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 21

acgcgtcgac tcccaggtcc agctgcagca g 31

<210> 22

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 22

gaaggtgtat ccagaagc 18

<210> 23

<211> 819

<212> DNA

<213> Mus

<220>

<221> CDS

<222> (1)...(813)

<223> pCHOM1. MABL1-scFv

<400> 23

atg gga tgg agc tgt atc atc ctc ttc ttg gta gca aca gct aca 45

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr

5

10

15

ggg gtc gac tcc cag gtc cag ctg cag cag tct gga cct gac ctg 90

Gly Val Asp Ser Gln Val Gln Leu Gln Gln Ser Gly Pro Asp Leu

20

25

30

gta aag cct ggg gct tca gtg aag atg tcc tgc aag gct tct gga 135

Val Lys Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly

35

40

45

tac acc ttc gtt aac cat gtt atg cac tgg gtg aag cag aag cca 180

Tyr Thr Phe Val Asn His Val Met His Trp Val Lys Gln Lys Pro

50

55

60

ggg cag ggc ctt gag tgg att gga tat att tat cct tac aat gat 225

Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Tyr Pro Tyr Asn Asp

65

70

75

ggg act aag tac aat gag aag ttc aag ggc aag gcc aca ctg act 270

Gly Thr Lys Tyr Asn Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr

80

85

90

tca gag aaa tcc tcc agc gca gcc tac atg gag ctc agc agc ctg 315

Ser Glu Lys Ser Ser Ser Ala Ala Tyr Met Glu Leu Ser Ser Leu

95

100

105

gcc tct gag gac tct gcg gtc tac tac tgt gca aga ggg ggt tac 360

Ala Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala Arg Gly Gly Tyr

110

115

120

tat agt tac gac gac tgg ggc caa ggc acc act ctc aca gtc tcc 405

Tyr Ser Tyr Asp Asp Trp Gly Gln Gly Thr Thr Leu Thr Val Ser

125

130

135

tca ggt ggt ggt ggt tcg ggt ggt ggt ggt tcg ggt ggt ggc gga 450

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly

140

145

150

tcg gat gtt gtg atg acc caa act cca ctc tcc ctg cct gtc agt 495

Ser Asp Val Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val Ser

155

160

165

ctt gga gat caa gcc tcc atc tct tgc aga tct agt cag agc ctt 540

Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu

170

175

180

cta cac agt aaa gga aac acc tat tta caa tgg tac cta cag aag 585

Leu His Ser Lys Gly Asn Thr Tyr Leu Gln Trp Tyr Leu Gln Lys

185

190

195

cca ggc cag tct cca aag ctc ctg atc tac aaa gtt tcc aac cga 630

Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg

200

205

210

TTT TCT GGG GTC CCA GAC AGG TTC AGT GGC AGT GGA TCA GGG ACA 675

Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr

215

220

225

gat ttc aca ctc aag atc agc aga gtg gag gct gag gat ctg gga 720

Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly

230

235

240

gtt tat ttc tgc tct caa agt aca cat gtt ccg tac acg tcc gga 765

Val Tyr Phe Cys Ser Gln Ser Thr His Val Pro Tyr Thr Ser Gly

245

250

255

ggg ggg acc aag ctg gaa ata aaa gac tac aaa gac gat gac gat 810

Gly Gly Thr Lys Leu Glu Ile Lys Asp Tyr Lys Asp Asp Asp Asp

260

265

270

aaa taa tga 819

Lys

<210> 24

<211> 828

<212> DNA

<213> Mus

<220>

<221> CDS

<222> (1)...(822)

<223> pscM2: MABL2-scFv

<400> 24

atg aaa tac cta ttg cct acg gca gcc gct gga ttg tta tta ctc 45

Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu

5

10

15

gct gcc caa cca gcc atg gcg cag gtc cag ctg cag cag tct gga 90

Ala Ala Gln Pro Ala Met Ala Gln Val Gln Leu Gln Gln Ser Gly

20

25

30

cct gaa ctg gta aag cct ggg gct tca gtg aag atg tcc tgc aag 135

Pro Glu Leu Val Lys Pro Gly Ala Ser Val Lys Met Ser Cys Lys

35

40

45

gct tct gga tac acc ttc gct aac cat gtt att cac tgg gtg aag 180

Ala Ser Gly Tyr Thr Phe Ala Asn His Val Ile His Trp Val Lys

50	55	60
cag aag cca ggg cag ggc ctt gag tgg att gga tat att tat cct 225		
Gln Lys Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Tyr Pro		
65	70	75
tac aat gat ggt act aag tat aat gag aag ttc aag gac aag gcc 270		
Tyr Asn Asp Gly Thr Lys Tyr Asn Glu Lys Phe Lys Asp Lys Ala		
80	85	90
act ctg act tca gac aaa tcc tcc acc aca gcc tac atg gac ctc 315		
Thr Leu Thr Ser Asp Lys Ser Ser Thr Thr Ala Tyr Met Asp Leu		
95	100	105
agc agc ctg gcc tct gag gac tct gcg gtc tat tac tgt gca aga 360		
Ser Ser Leu Ala Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala Arg		
110	115	120
ggg ggt tac tat act tac gac gac tgg ggc caa ggc acc act ctc 405		
Gly Gly Tyr Tyr Thr Tyr Asp Asp Trp Gly Gln Gly Thr Thr Leu		
125	130	135
aca gtc tcc tca ggt ggt ggt ggt tgc ggt ggt ggt ggt tgc ggt 450		
Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly		
140	145	150
ggt ggc gga tgc gat gtt gtg atg acc caa agt cca ctc tcc ctg 495		
Gly Gly Gly Ser Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu		
155	160	165
cct gtc agt ctt gga gat caa gcc tcc atc tct tgc aga tca agt 540		
Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser		
170	175	180
cag agc ctt gtg cac agt aat gga aag acc tat tta cat tgg tac 585		
Gln Ser Leu Val His Ser Asn Gly Lys Thr Tyr Leu His Trp Tyr		
185	190	195

ctg cag aag cca ggc cag tct cca aaa ctc ctg atc tac aaa gtt 630

Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val

200

205

210

tcc aac cga ttt tct ggg gtc cca gac agg ttc agt ggc agt gga 675

Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly

215

220

225

tca gtg aca gat ttc aca ctc atg atc agc aga gtg gag gct gag 720

Ser Val Thr Asp Phe Thr Leu Met Ile Ser Arg Val Glu Ala Glu

230

235

240

gat ctg gga gtt tat ttc tgc tct caa agt aca cat gtt ccg tac 765

Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser Thr His Val Pro Tyr

245

250

255

acg ttc gga ggg ggg acc aag ctg gaa ata aaa gac tac aaa gac 810

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Asp Tyr Lys Asp

260

265

270

gat gac gat aaa taa tga 828

Asp Asp Asp Lys

<210> 25

<211> 819

<212> DNA

<213> Mus

<220>

<221> CDS

<222> (1)...(813)

<223> pCHOM2. MABL2-scFv

<400> 25

atg gga tgg agc tgt atc atc ctc ttc ttg gta gca aca gct aca 45

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr
5 10 15
ggt gtc gac tcc cag gtc cag ctg cag cag tct gga cct gaa ctg 90
Gly Val Asp Ser Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu
20 25 30
gta aag cct ggg gct tca gtg aag atg tcc tgc aag gct tct gga 135
Val Lys Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly
35 40 45
tac acc ttc gct aac cat gtt att cac tgg gtg aag cag aag cca 180
Tyr Thr Phe Ala Asn His Val Ile His Trp Val Lys Gln Lys Pro
50 55 60
ggg cag ggc ctt gag tgg att gga tat att tat cct tac aat gat 225
Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Tyr Pro Tyr Asn Asp
65 70 75
ggt act aag tat aat gag aag ttc aag gac aag gcc act ctg act 270
Gly Thr Lys Tyr Asn Glu Lys Phe Lys Asp Lys Ala Thr Leu Thr
80 85 90
tca gac aaa tcc tcc acc aca gcc tac atg gac ctc agc agc ctg 315
Ser Asp Lys Ser Ser Thr Thr Ala Tyr Met Asp Leu Ser Ser Leu
95 100 105
gcc tct gag gac tct gcg gtc tat tac tgt gca aga ggg ggt tac 360
Ala Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala Arg Gly Gly Tyr
110 115 120
tat act tac gac gac tgg ggc caa ggc acc act ctc aca gtc tcc 405
Tyr Thr Tyr Asp Asp Trp Gly Gln Gly Thr Thr Leu Thr Val Ser
125 130 135
tca ggt ggt ggt ggt tcg ggt ggt ggt ggt tcg ggt ggt ggc gga 450
Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly

140	145	150
tcg gat gtt gtg atg acc caa agt cca ctc tcc ctg cct gtc agt 495		
Ser Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Ser		
155	160	165
ctt gga gat caa gcc tcc atc tct tgc aga tca agt cag agc ctt 540		
Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu		
170	175	180
gtg cac agt aat gga aag acc tat tta cat tgg tac ctg cag aag 585		
Val His Ser Asn Gly Lys Thr Tyr Leu His Trp Tyr Leu Gln Lys		
185	190	195
cca ggc cag tct cca aaa ctc ctg atc tac aaa gtt tcc aac cga 630		
Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg		
200	205	210
ttt tct ggg gtc cca gac agg ttc agt ggc agt gga tca gtg aca 675		
Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Val Thr		
215	220	225
gat ttc aca ctc atg atc agc aga gtg gag gct gag gat ctg gga 720		
Asp Phe Thr Leu Met Ile Ser Arg Val Glu Ala Glu Asp Leu Gly		
230	235	240
gtt tat ttc tgc tct caa agt aca cat gtt ccg tac acg ttc gga 765		
Val Tyr Phe Cys Ser Gln Ser Thr His Val Pro Tyr Thr Phe Gly		
245	250	255
ggg ggg acc aag ctg gaa ata aaa gac tac aaa gac gat gac gat 810		
Gly Gly Thr Lys Leu Glu Ile Lys Asp Tyr Lys Asp Asp Asp Asp		
260	265	270
aaa taa tga 819		
Lys		

<210> 26

<211> 456

<212> DNA

<213> Mus

<220>

<221> CDS

<222> (1)...(450)

<223> pCHO-shIAP. Soluble human IAP

<400> 26

atg tgg ccc ctg gta gcg gcg ctg ttg ctg ggc tcg gcg tgc tgc 45

Met Trp Pro Leu Val Ala Ala Leu Leu Leu Gly Ser Ala Cys Cys

5

10

15

gga tca gct cag cta cta ttt aat aaa aca aaa tct gta gaa ttc 90

Gly Ser Ala Gln Leu Leu Phe Asn Lys Thr Lys Ser Val Glu Phe

20

25

30

acg ttt tgt aat gac act gtc gtc att cca tgc ttt gtt act aat 135

Thr Phe Cys Asn Asp Thr Val Val Ile Pro Cys Phe Val Thr Asn

35

40

45

atg gag gca caa aac act act gaa gta tac gta aag tgg aaa ttt 180

Met Glu Ala Gln Asn Thr Thr Glu Val Tyr Val Lys Trp Lys Phe

50

55

60

aaa gga aga gat att tac acc ttt gat gga gct cta aac aag tcc 225

Lys Gly Arg Asp Ile Tyr Thr Phe Asp Gly Ala Leu Asn Lys Ser

65

70

75

act gtc ccc act gac ttt agt agt gca aaa att gaa gtc tca caa 270

Thr Val Pro Thr Asp Phe Ser Ser Ala Lys Ile Glu Val Ser Gln

80

85

90

tta cta aaa gga gat gcc tct ttg aag atg gat aag agt gat gct 315

Leu Leu Lys Gly Asp Ala Ser Leu Lys Met Asp Lys Ser Asp Ala
 95 100 105
 gtc tca cac aca gga aac tac act tgt gaa gta aca gaa tta acc 360
 Val Ser His Thr Gly Asn Tyr Thr Cys Glu Val Thr Glu Leu Thr
 110 115 120
 aga gaa ggt gaa acg atc atc gag cta aaa tat cgt gtt gtt tca 405
 Arg Glu Gly Glu Thr Ile Ile Glu Leu Lys Tyr Arg Val Val Ser
 125 130 135
 tgg ttt tct cca aat gaa aat gac tac aag gac gac gat gac aag 450
 Trp Phe Ser Pro Asn Glu Asn Asp Tyr Lys Asp Asp Asp Asp Lys
 140 145 150
 tga tag 456

<210> 27

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 27

ggaattccat atgcaagtgc aacttcaaca gtctggacct gaactg 46

<210> 28

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 28

ggaattctca ttattttatt tccagcttgg t 31

<210> 29

<211> 741

<212> DNA

<213> Mus

<220>

<221> CDS

<222> (1)...(735)

<223> pscM2DEm02. MABL2-scFv

<400> 29

atg caa gtg caa ctt caa cag tct gga cct gaa ctg gta aag cct 45

Met Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro

5

10

15

ggg gct tca gtg aag atg tcc tgc aag gct tct gga tac acc ttc 90

Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe

20

25

30

gct aac cat gtt att cac tgg gtg aag cag aag cca ggg cag ggc 135

Ala Asn His Val Ile His Trp Val Lys Gln Lys Pro Gly Gln Gly

35

40

45

ctt gag tgg att gga tat att tat cct tac aat gat ggt act aag 180

Leu Glu Trp Ile Gly Tyr Ile Tyr Pro Tyr Asn Asp Gly Thr Lys

50

55

60

tat aat gag aag ttc aag gac aag gcc act ctg act tca gac aaa 225

Tyr Asn Glu Lys Phe Lys Asp Lys Ala Thr Leu Thr Ser Asp Lys

65

70

75

tcc tcc acc aca gcc tac atg gac ctc agc agc ctg gcc tct gag 270

Ser Ser Thr Thr Ala Tyr Met Asp Leu Ser Ser Leu Ala Ser Glu
 80 85 90
 gac tct gcg gtc tat tac tgt gca aga ggg ggt tac tat act tac 315
 Asp Ser Ala Val Tyr Tyr Cys Ala Arg Gly Gly Tyr Tyr Thr Tyr
 95 100 105
 gac gac tgg ggc caa ggc acc act ctc aca gtc tcc tca ggt ggt 360
 Asp Asp Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Gly Gly
 110 115 120
 ggt ggt tcg ggt ggt ggt ggt tcg ggt ggt ggc gga tcg gat gtt 405
 Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Val
 125 130 135
 gtg atg acc caa agt cca ctc tcc ctg cct gtc agt ctt gga gat 450
 Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Ser Leu Gly Asp
 140 145 150
 caa gcc tcc atc tct tgc aga tca agt cag agc ctt gtg cac agt 495
 Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
 155 160 165
 aat gga aag acc tat tta cat tgg tac ctg cag aag cca ggc cag 540
 Asn Gly Lys Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly Gln
 170 175 180
 tct cca aaa ctc ctg atc tac aaa gtt tcc aac cga ttt tct ggg 585
 Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly
 185 190 195
 gtc cca gac agg ttc agt ggc agt gga tca gtg aca gat ttc aca 630
 Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Val Thr Asp Phe Thr
 200 205 210
 ctc atg atc agc aga gtg gag gct gag gat ctg gga gtt tat ttc 675
 Leu Met Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe

215	220	225
tgc tct caa agt aca cat gtt ccg tac acg ttc gga ggg ggg acc 720		
Cys Ser Gln Ser Thr His Val Pro Tyr Thr Phe Gly Gly Gly Thr		
230	235	240
aag ctg gaa ata aaa taa tga 741		
Lys Leu Glu Ile Lys		

<210> 30

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 30

cagacagtgg ttcaaagt 18

<210> 31

<211> 72

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 31

cgcgctcgacc gatccgccac caccggaacc accaccaccc gaaccaccac caccttttat 60

ttccagcttg gt

72

<210> 32

<211> 1605

<212> DNA

<213> Mus

<220>

<221> CDS

<222> (1)...(1599)

<223> pCHOM2(Fv)2. MABL2-sc(Fv)2

<400> 32

atg gga tgg agc tgt atc atc ctc ttc ttg gta gca aca gct aca	45
Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr	
5 10 15	
ggt gtc gac tcc cag gtc cag ctg cag cag tct gga cct gaa ctg	90
Gly Val Asp Ser Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu	
20 25 30	
gta aag cct ggg gct tca gtg aag atg tcc tgc aag gct tct gga	135
Val Lys Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly	
35 40 45	
tac acc ttc gct aac cat gtt att cac tgg gtg aag cag aag cca	180
Tyr Thr Phe Ala Asn His Val Ile His Trp Val Lys Gln Lys Pro	
50 55 60	
ggg cag ggc ctt gag tgg att gga tat att tat cct tac aat gat	225
Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Tyr Pro Tyr Asn Asp	
65 70 75	
ggt act aag tat aat gag aag ttc aag gac aag gcc act ctg act	270
Gly Thr Lys Tyr Asn Glu Lys Phe Lys Asp Lys Ala Thr Leu Thr	
80 85 90	
tca gac aaa tcc tcc acc aca gcc tac atg gac ctc agc agc ctg	315
Ser Asp Lys Ser Ser Thr Thr Ala Tyr Met Asp Leu Ser Ser Leu	
95 100 105	

gcc tct gag gac tct gcg gtc tat tac tgt gca aga ggg ggt tac 360
 Ala Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala Arg Gly Gly Tyr
 110 115 120
 tat act tac gac gac tgg ggc caa ggc acc act ctc aca gtc tcc 405
 Tyr Thr Tyr Asp Asp Trp Gly Gln Gly Thr Thr Leu Thr Val Ser
 125 130 135
 tca ggt ggt ggt ggt tcg ggt ggt ggt ggt tcg ggt ggt ggc gga 450
 Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 140 145 150
 tcg gat gtt gtg atg acc caa agt cca ctc tcc ctg cct gtc agt 495
 Ser Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Ser
 155 160 165
 ctt gga gat caa gcc tcc atc tct tgc aga tca agt cag agc ctt 540
 Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu
 170 175 180
 gtg cac agt aat gga aag acc tat tta cat tgg tac ctg cag aag 585
 Val His Ser Asn Gly Lys Thr Tyr Leu His Trp Tyr Leu Gln Lys
 185 190 195
 cca ggc cag tct cca aaa ctc ctg atc tac aaa gtt tcc aac cga 630
 Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg
 200 205 210
 ttt tct ggg gtc cca gac agg ttc agt ggc agt gga tca gtg aca 675
 Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Val Thr
 215 220 225
 gat ttc aca ctc atg atc agc aga gtg gag gct gag gat ctg gga 720
 Asp Phe Thr Leu Met Ile Ser Arg Val Glu Ala Glu Asp Leu Gly
 230 235 240
 gtt tat ttc tgc tct caa agt aca cat gtt ccg tac acg ttc gga 765

Val Tyr Phe Cys Ser Gln Ser Thr His Val Pro Tyr Thr Phe Gly			
245	250	255	
ggg ggg acc aag ctg gaa ata aaa ggt ggt ggt ggt tgc ggt ggt	810		
Gly Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly			
260	265	270	
ggt ggt tgc ggt ggt ggc gga tgc gtc gac tcc cag gtc cag ctg	855		
Gly Gly Ser Gly Gly Gly Gly Ser Val Asp Ser Gln Val Gln Leu			
275	280	285	
cag cag tct gga cct gaa ctg gta aag cct ggg gct tca gtg aag	900		
Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala Ser Val Lys			
290	295	300	
atg tcc tgc aag gct tct gga tac acc ttc gct aac cat gtt att	945		
Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ala Asn His Val Ile			
305	310	315	
cac tgg gtg aag cag aag cca ggg cag ggc ctt gag tgg att gga	990		
His Trp Val Lys Gln Lys Pro Gly Gln Gly Leu Glu Trp Ile Gly			
320	325	330	
tat att tat cct tac aat gat ggt act aag tat aat gag aag ttc	1035		
Tyr Ile Tyr Pro Tyr Asn Asp Gly Thr Lys Tyr Asn Glu Lys Phe			
335	340	345	
aag gac aag gcc act ctg act tca gac aaa tcc tcc acc aca gcc	1080		
Lys Asp Lys Ala Thr Leu Thr Ser Asp Lys Ser Ser Thr Thr Ala			
350	355	360	
tac atg gac ctc agc agc ctg gcc tct gag gac tct gcg gtc tat	1125		
Tyr Met Asp Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val Tyr			
365	370	375	
tac tgt gca aga ggg ggt tac tat act tac gac gac tgg ggc caa	1170		
Tyr Cys Ala Arg Gly Gly Tyr Tyr Thr Tyr Asp Asp Trp Gly Gln			

380	385	390
ggc acc act ctc aca gtc tcc tca ggt ggt ggt ggt tgc ggt ggt 1215		
Gly Thr Thr Leu Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly		
395	400	405
ggt ggt tgc ggt ggt ggc gga tgc gat gtt gtg atg acc caa agt 1260		
Gly Gly Ser Gly Gly Gly Gly Ser Asp Val Val Met Thr Gln Ser		
410	415	420
cca ctc tcc ctg cct gtc agt ctt gga gat caa gcc tcc atc tct 1305		
Pro Leu Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser		
425	430	435
tgc aga tca agt cag agc ctt gtg cac agt aat gga aag acc tat 1350		
Cys Arg Ser Ser Gln Ser Leu Val His Ser Asn Gly Lys Thr Tyr		
440	445	450
tta cat tgg tac ctg cag aag cca ggc cag tct cca aaa ctc ctg 1395		
Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu		
455	460	465
atc tac aaa gtt tcc aac cga ttt tct ggg gtc cca gac agg ttc 1440		
Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe		
470	475	480
agt ggc agt gga tca gtg aca gat ttc aca ctc atg atc agc aga 1485		
Ser Gly Ser Gly Ser Val Thr Asp Phe Thr Leu Met Ile Ser Arg		
485	490	495
gtg gag gct gag gat ctg gga gtt tat ttc tgc tct caa agt aca 1530		
Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser Thr		
500	505	510
cat gtt ccg tac acg ttc gga ggg ggg acc aag ctg gaa ata aaa 1575		
His Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys		
515	520	525

gac tac aaa gac gat gac gat aaa taa tga 1605

Asp Tyr Lys Asp Asp Asp Asp Lys

530

<210> 33

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 33

tgaggaattc ccaccatggg atg 23

<210> 34

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 34

cacgacgtca ctgagactg tgagagtggg gccttgccc 40

<210> 35

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 35

agtctcgagt gacgtcgtga tgacccaaag tccactctcc 40

<210> 36

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 36

gactggatcc tcattattta tcgtcatcgt c 31

<210> 37

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 37

cgcgtaatac gactcactat ag 22

<210> 38

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 38

gcaattggac ctgttttatac tcgagcttgg tccccctcc gaacgt 46

<210> 39

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 39

gctcgagata aaacaggtcc aattgcagca gtctggacct gaact 45

<210> 40

<211> 60

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 40

gactggatcc tcattattta tcgtcatcgt cttttagtc tgaggagact gtgagagtgg 60

<210> 41

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 41

gactgaattc ccacatgaa gttgcctgtt ag 32

<210> 42

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 42

cagtctcgag tgggtggttcc gacgtcgtga tgacccaaag 40

<210> 43

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 43

cagtctcgag tgggtggtggt tccgacgtcg tgatgaccca aag 43

<210> 44

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 44

cagtctcgag tgggtggtggt ggttccgacg tcgtgatgac ccaaag 46

<210> 45

<211> 49

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 45

cagtctcgag tgggtggtggt ggtggttccg acgtcgtgat gacccaaag 49

<210> 46

<211> 52

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 46

cagtctcgag tgggtggtggt ggtggtggtt ccgacgtcgt gatgacccaa ag 52

<210> 47

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 47

ggccgcatgt tgtcacgaat 20

<210> 48

<211> 780

<212> DNA

<213> Mus

<220>

<221> CDS

<222> (1)...(768)

<223> CF2HL-0/pCOS1. MABL2-scFv<HL-0>

<400> 48

atg gga tgg agc tgt atc atc ctc ttc ttg gta gca aca gct aca ggt gtc 51

MET Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly Val

5

10

15

gac tcc cag gtc cag ctg cag cag tct gga cct gaa ctg gta aag cct ggg 102

Asp Ser Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly

20

25

30

gct tca gtg aag atg tcc tgc aag gct tct gga tac acc ttc gct aac cat 153

Ala Ser Val Lys MET Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ala Asn His

35

40

45

50

gtt att cac tgg gtg aag cag aag cca ggg cag ggc ctt gag tgg att gga 204

Val Ile His Trp Val Lys Gln Lys Pro Gly Gln Gly Leu Glu Trp Ile Gly

55

60

65

tat att tat cct tac aat gat ggt act aag tat aat gag aag ttc aag gac 255

Tyr Ile Tyr Pro Tyr Asn Asp Gly Thr Lys Tyr Asn Glu Lys Phe Lys Asp

70

75

80

85

aag gcc act ctg act tca gac aaa tcc tcc acc aca gcc tac atg gac ctc 306

Lys Ala Thr Leu Thr Ser Asp Lys Ser Ser Thr Thr Ala Tyr MET Asp Leu

90

95

100

agc agc ctg gcc tct gag gac tct gcg gtc tat tac tgt gca aga ggg ggt 357

Ser Ser Leu Ala Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala Arg Gly Gly

105 110 115
 tac tat act tac gac gac tgg ggc caa ggc acc act ctc aca gtc tcg agt 408
 Tyr Tyr Thr Tyr Asp Asp Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser
 120 125 130 135
 gac gtc gtg atg acc caa agt cca ctc tcc ctg cct gtc agt ctt gga gat 459
 Asp Val Val MET Thr Gln Ser Pro Leu Ser Leu Pro Val Ser Leu Gly Asp
 140 145 150
 caa gcc tcc atc tct tgc aga tca agt cag agc ctt gtg cac agt aat gga 510
 Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser Asn Gly
 155 160 165 170
 aag acc tat tta cat tgg tac ctg cag aag cca ggc cag tct cca aaa ctc 561
 Lys Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu
 175 180 185
 ctg atc tac aaa gtt tcc aac cga ttt tct ggg gtc cca gac agg ttc agt 612
 Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser
 190 195 200
 ggc agt gga tca gtg aca gat ttc aca ctc atg atc agc aga gtg gag gct 663
 Gly Ser Gly Ser Val Thr Asp Phe Thr Leu MET Ile Ser Arg Val Glu Ala
 205 210 215 220
 gag gat ctg gga gtt tat ttc tgc tct caa agt aca cat gtt ccg tac acg 714
 Glu Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser Thr His Val Pro Tyr Thr
 225 230 235
 ttc gga ggg ggg acc aag ctg gaa ata aaa gac tac aaa gac gat gac gat 765
 Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Asp Tyr Lys Asp Asp Asp Asp
 240 245 250 255
 aaa taa tga gga tcc 780
 Lys

<210> 49

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 49

caagctcgag ataaaatccg gaggccaggt ccaattgcag cagtc 45

<210> 50

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 50

caagctcgag ataaaatccg gaggtggcca ggtccaattg cagcagtc 48

<210> 51

<211> 51

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 51

caagctcgag ataaaatccg gaggtggtgg ccaggtccaa ttgcagcagt c 51

<210> 52

<211> 54

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 52

caagctcgag ataaaatccg gaggtggtgg tggccaggtc caattgcagc agtc 54

<210> 53

<211> 57

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 53

caagctcgag ataaaatccg gaggtggtgg tggcggccag gtccaattgc agcagtc 57

<210> 54

<211> 780

<212> DNA

<213> Mus

<220>

<221> CDS

<222> (1)...(768)

<223> CF2LH-0/pCOS1. MABL2-scFv<LH-0>

<400> 54

atg aag ttg cct gtt agg ctg ttg gtg ctg atg ttc tgg att cct ggt tcc 51

MET Lys Leu Pro Val Arg Leu Leu Val Leu MET Phe Trp Ile Pro Gly Ser

5	10	15	
agc agt gat gtt gtg atg acc caa agt cca ctc tcc ctg cct gtc agt ctt 102			
Ser Ser Asp Val Val MET Thr Gln Ser Pro Leu Ser Leu Pro Val Ser Leu			
20	25	30	
gga gat caa gcc tcc atc tct tgc aga tca agt cag agc ctt gtg cac agt 153			
Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser			
35	40	45	50
aat gga aag acc tat tta cat tgg tac ctg cag aag cca ggc cag tct cca 204			
Asn Gly Lys Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro			
55	60	65	
aaa ctc ctg atc tac aaa gtt tcc aac cga ttt tct ggg gtc cca gac agg 255			
Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg			
70	75	80	85
ttc agt ggc agt gga tca gtg aca gat ttc aca ctc atg atc agc aga gtg 306			
Phe Ser Gly Ser Gly Ser Val Thr Asp Phe Thr Leu MET Ile Ser Arg Val			
90	95	100	
gag gct gag gat ctg gga gtt tat ttc tgc tct caa agt aca cat gtt ccg 357			
Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser Thr His Val Pro			
105	110	115	
tac acg ttc gga ggg ggg acc aag ctc gag ata aaa cag gtc caa ttg cag 408			
Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gln Val Gln Leu Gln			
120	125	130	135
cag tct gga cct gaa ctg gta aag cct ggg gct tca gtg aag atg tcc tgc 459			
Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala Ser Val Lys MET Ser Cys			
140	145	150	
aag gct tct gga tac acc ttc gct aac cat gtt att cac tgg gtg aag cag 510			
Lys Ala Ser Gly Tyr Thr Phe Ala Asn His Val Ile His Trp Val Lys Gln			
155	160	165	170

aag cca ggg cag ggc ctt gag tgg att gga tat att tat cct tac aat gat 561

Lys Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Tyr Pro Tyr Asn Asp

175

180

185

ggt act aag tat aat gag aag ttc aag gac aag gcc act ctg act tca gac 612

Gly Thr Lys Tyr Asn Glu Lys Phe Lys Asp Lys Ala Thr Leu Thr Ser Asp

190

195

200

aaa tcc tcc acc aca gcc tac atg gac ctc agc agc ctg gcc tct gag gac 663

Lys Ser Ser Thr Thr Ala Tyr MET Asp Leu Ser Ser Leu Ala Ser Glu Asp

205

210

215

220

tct gcg gtc tat tac tgt gca aga ggg ggt tac tat act tac gac gac tgg 714

Ser Ala Val Tyr Tyr Cys Ala Arg Gly Gly Tyr Tyr Thr Tyr Asp Asp Trp

225

230

235

ggc caa ggc acc act ctc aca gtc tcc tca gac tac aaa gac gat gac gat 765

Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Asp Tyr Lys Asp Asp Asp Asp

240

245

250

255

aaa taa tga gga tcc 780

Lys

<210> 55

<211> 351

<212> DNA

<213> Human

<220>

<221> CDS

<222> (1)...(351)

<223> 12B5HV. 1-351 peptide

<400> 55

cag gtg cag ctg gtg cag tct ggg gga ggc ttg gtc cgg ccc ggg ggg tcc ctg agt ctc 60

Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Arg Pro Gly Gly Ser Leu Ser Leu
 5 10 15 20
 tcc tgt gca gtc tct gga atc acc ctc agg acc tac ggc atg cac tgg gtc cgc cag gct 120
 Ser Cys Ala Val Ser Gly Ile Thr Leu Arg Thr Tyr Gly MET His Trp Val Arg Gln Ala
 25 30 35 40
 cca ggc aag ggg ctg gag tgg gtg gca ggt ata tcc ttt gac gga aga agt gaa tac tat 180
 Pro Gly Lys Gly Leu Glu Trp Val Ala Gly Ile Ser Phe Asp Gly Arg Ser Glu Tyr Tyr
 45 50 55 60
 gca gac tcc gtg cag ggc cga ttc acc atc tcc aga gac agt tcc aag aac acc ctg tat 240
 Ala Asp Ser Val Gln Gly Arg Phe Thr Ile Ser Arg Asp Ser Ser Lys Asn Thr Leu Tyr
 65 70 75 80
 ctg caa atg aac agc ctg aga gcc gag gac acg gct gtg tat tac tgt gcg aga gga gca 300
 Leu Gln MET Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Gly Ala
 85 90 95 100
 cat tat ggt ttc gat atc tgg ggc caa ggg aca atg gtc acc gtc tcg agt 351
 His Tyr Gly Phe Asp Ile Trp Gly Gln Gly Thr MET Val Thr Val Ser Ser
 105 110 115

<210> 56

<211> 57

<212> DNA

<213> Human

<220>

<221> CDS

<222> (1)...(57)

<223> reader sequence

<400> 56

atg gag ttt ggg ctg agc tgg gtt ttc ctc gtt gct ctt tta aga ggt gtc cag tgt 57

MET Glu Phe Gly Leu Ser Trp Val Phe Leu Val Ala Leu Leu Arg Gly Val Gln Cys

5

10

15

<210> 57

<211> 115

<212> DNA

<213> Artificial Sequence

<220>

<223> 12B5VH-1

<400> 57

atggagtttg ggctgagctg ggttttcctc gttgctcttt taagaggtgt ccagtgtcag 60

gtgcagctgg tgcagtctgg gggaggcttg gtccggcccg gggggtccct gagtc 115

<210> 58

<211> 115

<212> DNA

<213> Artificial Sequence

<220>

<223> 12B5VH-2

<400> 58

aaggatatac ctgccacca ctccagcccc ttgcctggag cctggcggac ccagtgcattg 60

ccgtaggtcc tgagggtgat tccagagact gcacaggaga gactcaggga ccccc 115

<210> 59

<211> 115

<212> DNA

<213> Artificial Sequence

<220>

<223> 12B5VH-3

<400> 59

ggcaggtata tcctttgacg gaagaagtga atactatgca gactccgtgc agggccgatt 60
caccatctcc agagacagtt ccaagaacac cctgtatctg caaatgaaca gcctg 115

<210> 60

<211> 115

<212> DNA

<213> Artificial Sequence

<220>

<223> 12B5VH-4

<400> 60

actcgagacg gtgaccattg tcccttgcc ccagatatcg aaaccataat gtgctcctct 60
cgcacagtaa tacacagccg tgtcctcggc tctcaggetg ttcatttg 108

<210> 61

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> 12B5VH-S, PCR primer

<400> 61

ttcaagcttc caccatggag tttgggctga gc 32

<210> 62

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> 12B5VH-A, PCR primer

<400> 62

ttgggatcca ctcaccactc gagacggtga ccat 34

<210> 63

<211> 433

<212> DNA

<213> Human

<220>

<221> CDS

<222> (12)...(419)

<223> HEF-12B5H-g gamma. 12-419 peptide

<400> 63

aagcttccac c atg gag ttt ggg ctg agc tgg gtt ttc ctc gtt gct ctt tta aga 56

MET Glu Phe Gly Leu Ser Trp Val Phe Leu Val Ala Leu Leu Arg

1

5

10

15

ggg gtc cag tgt cag gtg cag ctg gtg cag tct ggg gga ggc ttg gtc cgg ccc ggg ggg 116

Gly Val Gln Cys Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Arg Pro Gly Gly

20

25

30

35

tcc ctg agt ctc tcc tgt gca gtc tct gga atc acc ctc agg acc tac ggc atg cac tgg 176

Ser Leu Ser Leu Ser Cys Ala Val Ser Gly Ile Thr Leu Arg Thr Tyr Gly MET His Trp

40

45

50

55

gtc cgc cag gct cca ggc aag ggg ctg gag tgg gtg gca ggt ata tcc ttt gac gga aga 236

Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Gly Ile Ser Phe Asp Gly Arg

60

65

70

75

agt gaa tac tat gca gac tcc gtg cag ggc cga ttc acc atc tcc aga gac agt tcc aag 296

Ser Glu Tyr Tyr Ala Asp Ser Val Gln Gly Arg Phe Thr Ile Ser Arg Asp Ser Ser Lys

80	85	90	95
aac acc ctg tat ctg caa atg aac agc ctg aga gcc gag gac acg gct gtg tat tac tgt 356			
Asn Thr Leu Tyr Leu Gln MET Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys			
100	105	110	115
gcg aga gga gca cat tat ggt ttc gat atc tgg ggc caa ggg aca atg gtc acc gtc tcg 416			
Ala Arg Gly Ala His Tyr Gly Phe Asp Ile Trp Gly Gln Gly Thr MET Val Thr Val Ser			
120	125	130	135
agt ggtgagtga tcc 433			
Ser			

<210> 64

<211> 323

<212> DNA

<213> Human

<220>

<221> CDS

<222> (1)...(323)

<223> 12B5LV. 1-323 peptide

<400> 64

gac atc cag atg acc cag tct cct tcc acc ctg tct gca tct att gga gac aga gtc acc 60			
Asp Ile Gln MET Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Ile Gly Asp Arg Val Thr			
5	10	15	20
atc acc tgc cgg gcc agc gag ggt att tat cac tgg ttg gcc tgg tat cag cag aag cca 120			
Ile Thr Cys Arg Ala Ser Glu Gly Ile Tyr His Trp Leu Ala Trp Tyr Gln Gln Lys Pro			
25	30	35	40
ggg aaa acc cct aaa ctc ctg atc tat aag gcc tct agt tta gcc agt ggg gcc cca tca 180			
Gly Lys Ala Pro Lys Leu Leu Ile Tyr Lys Ala Ser Ser Leu Ala Ser Gly Ala Pro Ser			
45	50	55	60

agg ttc agc ggc agt gga tct ggg aca gat ttc act ctc acc atc agc agc ctg cag cct 240

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

65

70

75

80

gat gat ttt gca act tat tac tgc caa caa tat agt aat tat ccg ctc act ttc ggc gga 300

Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Asn Tyr Pro Leu Thr Phe Gly Gly

85

90

95

100

ggg acc aag ctg gag atc aaa 323

Gly Thr Lys Leu Glu Ile Lys

105

<210> 65

<211> 66

<212> DNA

<213> Human

<220>

<221> CDS

<222> (1)...(57)

<223> reader sequence

<400> 65

atg gac atg agg gtc ccc gct cag ctc ctg ggg ctc ctg ctg ctc tgg ctc cca ggt gcc 60

MET Asp MET Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp Leu Pro Gly Ala

5

10

15

20

Aaa tgt 66

Lys Cys

<210> 66

<211> 110

<212> DNA

<213> Artificial Sequence

<220>

<223> 12B5VL-1

<400> 66

atggacatga gggccccgc tcagctcctg gggctcctgc tgctctggct cccagggtgcc 60
aaatgtgaca tccagatgac ccagtcctct tccaccctgt ctgcatttat 110

<210> 67

<211> 110

<212> DNA

<213> Artificial Sequence

<220>

<223> 12B5VL-2

<400> 67

ggagtttagg ggctttccct ggctttctgt gataccaggc caaccagtga taaataccct 60
cgctggcccg gcaggatgat gtgactctgt ctccaataga tgcagacagg 110

<210> 68

<211> 110

<212> DNA

<213> Artificial Sequence

<220>

<223> 12B5VL-3

<400> 68

aagcccctaa actcctgac tataaggcct ctagttagc cagtggggcc ccatcaaggt 60
tcagcggcag tggatctggg acagatttca ctctacccat cagcagcctg 110

<210> 69

<211> 110

<212> DNA

<213> Artificial Sequence

<220>

<223> 12B5VL-4

<400> 69

accatcagca gctgcagcc tgatgatttt gcaacttatt actgccaaca atatagtaat 60
tatccgctca ctttcggcgg agggaccaag ctggagatca aa 102

<210> 70

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> 12B5VL-S, PCR primer

<400> 70

ttcaagcttc caccatggac atgagggtcc cc 32

<210> 71

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> 12B5VL-A, PCR primer

<400> 71

tctaggatcc actcacgttt gatctccagc ttggt 35

<210> 72

<211> 415

<212> DNA

<213> Human

<220>

<221> CDS

<222> (12)...(398)

<223> HEF-12B5H-g kappa. 12-398 peptide

<400> 72

aagcttcac c atg gac atg agg gtc ccc gct cag ctc ctg ggg ctc ctg ctg ctc 56

MET Asp MET Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu

1

5

10

15

tgg ctc cca ggt gcc aaa tgt gac atc cag atg acc cag tct cct tcc acc ctg tct gca 116

Trp Leu Pro Gly Ala Lys Cys Asp Ile Gln MET Thr Gln Ser Pro Ser Thr Leu Ser Ala

20

25

30

35

tct att gga gac aga gtc acc atc acc tgc cgg gcc agc gag ggt att tat cac tgg ttg 176

Ser Ile Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Glu Gly Ile Tyr His Trp Leu

40

45

50

55

gcc tgg tat cag cag aag cca ggg aaa gcc cct aaa ctc ctg atc tat aag gcc tct agt 236

Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Lys Ala Ser Ser

60

65

70

75

tta gcc agt ggg gcc cca tca agg ttc agc ggc agt gga tct ggg aca gat ttc act ctc 296

Leu Ala Ser Gly Ala Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu

80

85

90

95

acc atc agc agc ctg cag cct gat gat ttt gca act tat tac tgc caa caa tat agt aat 356

Thr Ile Ser Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Asn

100

105

110

115

tat ccg ctc act ttc ggc gga ggg acc aag ctg gag atc aaa cgtgagtgga tcctaga 415

Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys

120

125